



THE UNITED STATES PATENT AND TRADEMARK OFFICE

Applicant: Marc Albertsen et al.	1	Art Unit: 1638
Serial No.: 10/021,657	1	
Filed: December 14, 2001	1	Examiner: A. Kubelik
For: Nucleotide Sequences Mediating Fertility and Method of Using Same	1	Confirmation No. 5787

DECLARATION UNDER 37 CFR §1.131

Commissioner for Patents  
Washington, D.C. 20231  
Sir:

I, Tim Fox, declare and say:


I am an inventor for the above-identified application. I conceived and reduced to practice in the United States the invention claimed in the above-identified patent application prior to February, 2000, the publishing date of the reference to Genbank accession AW424821.2; prior to March, 2000, the publishing date of the reference to Genbank accession AW519943; and prior to August 2000, the publishing date of the reference to Genbank accession BE494080.1. Attached Exhibit A is the sequence of the SBMu200 gene, which sequencing was conducted at my instructions by our contractor and provided to before the dates identified above.

The invention was thus conceived and reduced to practice in the United States prior to February 2000. The Exhibit, which relates to the conception and actual reduction to practice, corresponds to the invention broadly disclosed and claimed in the above-identified application.

The undersigned declares further that all statements made herein of his own knowledge are true and all statements made on information and belief are believed to be true; and further that these statements were made with the knowledge that willful, false statements and the like so made are punishable by fine or imprisonment, or both, under Section 1001 of title 18 United States Code and that such willful false statements may jeopardize the validity of the application or any patents issuing thereon.

10/18/04

Date



Tim Fox

USSN 10/021,657  
Exhibit A

(Linear) MAP of: Sb20081.Seq check: 1232 from: 1 to: 1906

REFORMAT of: Sb20081.Seq check: -1 from: 1 to: 1912 10:59  
TASSEL SPECIFIC cDNA ISOLATED FROM MAIZE INBRED A632. THIS CLONE IS MISSING  
THE FIRST MET, WHICH MAY BE DUE TO CLONING ARTIFACT AS COMPARED TO THE GENOMIC.  
cDNA LIBRARY MADE FROM MAIZE TASSEL mRNA IN UNI-ZAP VECTOR (STRATAGENE).  
SEQUENCING DONE BY LOFTSTRAND AND IS DOUBLE STRAND VERIFIED.

With 2 enzymes: ECORI XHOI

████████████████████ ..

EcoRI  
|  
GAATTCGGGCACGAGGGAAGCTCACCTCACGCCGGCGACGCCATCGCCATTCTTCCCCTA  
1 -----+-----+-----+-----+-----+-----+ 60  
CTTAAGCCGTGCTCCCTTCGAGTGGAGTGCGCCGCTGCGGTAGCGGTAAGAAGGGTGAT

a E F G T R E A H L T P A T P S P F F P L -

GCAGGGCCTCACAAGTACATCGCGCTCCTTCTGGTTGTCCTCTCATGGATCCTGGTCCAG  
61 -----+-----+-----+-----+-----+ 120  
CGTCCCGGAGTGTTTCATGTAGCGCGAGGAAGACCAACAGGAGAGTACCTAGGACCAGGTC

a A G P H K Y I A L L L V V L S W I L V Q -

AGGTGGAGCCTGAGGAAGCAGAAAGGCCGAGATCATGGCCAGTCATCGGCGCAACGGTG  
121 -----+-----+-----+-----+-----+ 180  
TCCACCTCGGACTCCTTCGTCTTCCGGGCTCTAGTACCGGTGAGTACCGCGTTGCCAC

a R W S L R K Q K G P R S W P V I G A T V -

GAGCAGCTGAGGAACCTACCACCGGATGCACGACTGGCTTGTCGGGTACCTGTACGGCAC  
181 -----+-----+-----+-----+-----+ 240  
CTCGTCGACTCCTTGATGGTGGCTACGTGCTGACCGAACAGCCCATGGACAGTGGCGTG

a E Q L R N Y H R M H D W L V G Y L S R H -

AGGACAGTGACCGTCGACATGCCGTTCACTTCTACACCTACATCGCTGACCCGGTGAAT  
241 -----+-----+-----+-----+-----+ 300  
TCCTGTCACTGGCAGCTGTACGGCAAGTGAAGGATGTGGATGTAGCGACTGGGCCACTTA

a R T V T V D M P F T S Y T Y I A D P V N -

GTCGAGCATGTCTCAAGACTAACTTCACCAATTACCCCAAGGGAATCGTGACAGATCC  
301 -----+-----+-----+-----+-----+ 360  
CAGCTCGTACAGGAGTTCTGATTGAAGTGGTTAATGGGGTTCCCTTAGCACATGTCTAGG

a V E H V L K T N F T N Y P K G I V Y R S -

TACATGGACGTGCTCCTCGGTGACGGCATCTTCAACGCCGACGGCGAGCTGTGGAGGAAG  
361 -----+-----+-----+-----+-----+ 420  
ATGTACCTGCACGAGGAGCCACTGCCGTAGAAGTTGCGGCTGCCGCTCGACACCTCCTTC

a Y M D V L L G D G I F N A D G E L W R K -

CAGAGGAAGACGGCGAGTTTCGAGTTCGCCTCCAAGAACCTGAGGGATTTACAGCGCCATT  
421 -----+-----+-----+-----+-----+ 480  
GTCTCCTTCTGCCGCTCAAAGCTCAAGCGGAGGTTCTTGGACTCCCTAAAGTCGCGGTAA

a Q R K T A S F E F A S K N L R D F S A I -

481 GTGTTTCAGAGAGTACTCCCTGAAGCTGTCGGGTATACTGAGCCAGGCATCCAAGGCAGGC  
 -----+-----+-----+-----+-----+-----+-----+ 540  
 CACAAGTCTCTCATGAGGGACTTCGACAGCCCATATGACTCGGTCCGTAGGTCCGTCCG  
  
 a V F R E Y S L K L S G I L S Q A S K A G -  
  
 541 AAAGTTGTGGACATGCAGGAACTTTACATGAGGATGACGCTGGACTCCATCTGCAAGGTT  
 -----+-----+-----+-----+-----+-----+ 600  
 TTTCAACACCTGTACGTCTTGAAATGTACTCCTACTGCGACCTGAGGTAGACGTTCCAA  
  
 a K V V D M Q E L Y M R M T L D S I C K V -  
  
 601 GGGTTCGGGGTCGAGATCGGCACGCTGTCGCCAGATCTCCCCGAGAACAGCTTCGCGCAG  
 -----+-----+-----+-----+-----+-----+ 660  
 CCCAAGCCCCAGCTCTAGCCGTGCGACAGCGGTCTAGAGGGGCTCTGTGCGAAGCGCGTC  
  
 a G F G V E I G T L S P D L P E N S F A Q -  
  
 661 GCGTTCGATGCCGCCAACATCATCATCACGCTGCGGTTTCATCGACCCGCTGTGGCGCATC  
 -----+-----+-----+-----+-----+-----+ 720  
 CGCAAGCTACGGCGGTTGTAGTAGTAGTGCGACGCCAAGTAGCTGGGCGACACCGCGTAG  
  
 a A F D A A N I I I T L R F I D P L W R I -  
  
 721 AAGAGTTTCTTCCACGTCGGGTCAGAGGCCCTCCTAGCGCAGAGCATCAAGCTCGTGGAC  
 -----+-----+-----+-----+-----+-----+ 780  
 TTCTCCAAGAAGGTGCAGCCCAGTCTCCGGGAGGATCGCGTCTCGTAGTTCGAGCACCTG  
  
 a K R F F H V G S E A L L A Q S I K L V D -  
  
 781 GAGTTCACCTACAGCGTGATCCGCCGGAGGAAGGCCGAGATCGTCGAGGTCCGGGCCAGC  
 -----+-----+-----+-----+-----+-----+ 840  
 CTCAAGTGGATGTCGCACTAGGCGGCCTCCTTCCGGCTCTAGCAGCTCCAGGCCCGGTG  
  
 a E F T Y S V I R R R K A E I V E V R A S -  
  
 841 GGCAAACAGGAGAAGATGAAGCACGACATCCTGTCACGGTTCATCGAGCTGGGCGAGGCC  
 -----+-----+-----+-----+-----+-----+ 900  
 CCGTTTGTCTCTTCTACTTCGTGCTGTAGGACAGTGCCAAGTAGCTCGACCCGCTCCGG  
  
 a G K Q E K M K H D I L S R F I E L G E A -  
  
 901 GGCGACGACGGCGCGGCTTCGGGGACGATAAGAGCCTCCGGGACGTGGTGCTCAACTTC  
 -----+-----+-----+-----+-----+-----+ 960  
 CCGCTGCTGCCGCCGCCGAAGCCCCTGCTATTCTCGGAGGCCCTGCACCACGAGTTGAAG  
  
 a G D D G G G F G D D K S L R D V V L N F -  
  
 961 GTGATCGCCGGGCGGGACACGACGGCGACGACGCTGTCGTGGTTCACGCACATGGCCATG  
 -----+-----+-----+-----+-----+-----+ 1020  
 CACTAGCGGCCCCCCTGTGCTGCCGCTGTGCGACAGCACCAAGTGCGTGTACCGGTAC  
  
 a V I A G R D T T A T T L S W F T H M A M -  
  
 1021 TCCACCCGACGCTGGCCGAGAAGCTGCGCCGAGCTGTGCGCGTTCGAGGCGGAGCGC  
 -----+-----+-----+-----+-----+-----+ 1080  
 AGGGTGGGCCTGCACCGGCTCTTCGACGCGGCGCTCGACACGCGCAAGCTCCGCCTCGCG  
  
 a S H P D V A E K L R R E L C A F E A E R -

1081 GCGCGCGAGGAGGGCGTCACGCTCGTGCTCTGCGGCGGCGCTGACGCCGACGACAAGGCG 1140  
 -----+-----+-----+-----+-----+-----+  
 CGCGCGCTCCTCCCGCAGTGCGAGCACGAGACGCCGCCGCGACTGCGGCTGCTGTTCCGC  
 a A R E E G V T L V L C G G A D A D D K A -  
 TTCGCCGCCCCGCGTGGCGCAGTTCGCGGGCCTCCTCACCTACGACAGCCTCGGCAAGCTG  
 1141 -----+-----+-----+-----+-----+-----+ 1200  
 AAGCGGCGGGCGCACCGCGTCAAGCGCCCCGAGGAGTGGATGCTGTGCGAGCCGTTTCGAC  
 a F A A R V A Q F A G L L T Y D S L G K L -  
 GTCTACCTCCACGCCTGCGTCACCGAGACGCTCCGCCTGTACCCCGCCGTCCCTCAGGAC  
 1201 -----+-----+-----+-----+-----+-----+ 1260  
 CAGATGGAGGTGCGGACGCAGTGGCTCTGCGAGGCGGACATGGGGCGGCAGGGAGTCTTG  
 a V Y L H A C V T E T L R L Y P A V P Q D -  
 CCCAAGGGGATCCTGGAGGACGACGTGCTGCCGGACGGGACGAAGGTGAGGGCCGGCGGG  
 1261 -----+-----+-----+-----+-----+-----+ 1320  
 GGGTTCCTTAGGACCTCCTGCTGCACGACGGCCTGCCCTGCTTCCACTCCCGGCCGCC  
 a P K G I L E D D V L P D G T K V R A G G -  
 ATGGTGACGTACGTGCCCTACTCGATGGGGCGGATGGAGTACAACGGGGCCCCGACGCG  
 1321 -----+-----+-----+-----+-----+-----+ 1380  
 TACCACTGCATGCACGGGATGAGCTACCCCGCTACCTCATGTTGACCCCGGGGCTGCGC  
 a M V T Y V P Y S M G R M E Y N W G P D A -  
 GCGAGCTTCCGGCCGGAGCGGTGGATCAACGAGGATGGCGCGTTCCGCAACGCGTCGCCC  
 1381 -----+-----+-----+-----+-----+-----+ 1440  
 CGCTCGAAGGCCGGCCTCGCCACCTAGTTGCTCCTACCGCGCAAGGCGTTGCGCAGCGGC  
 a A S F R P E R W I N E D G A F R N A S P -  
 TTCAAGTTCACGGCGTTCCAGGCGGGGCCGAGGATCTGCCTGGGCAAGGACTCGGCGTAC  
 1441 -----+-----+-----+-----+-----+-----+ 1500  
 AAGTTCAAGTGCCGCAAGGTCCGCCCCGGCTCCTAGACGACCCGTTCTGAGCCGCATG  
 a F K F T A F Q A G P R I C L G K D S A Y -  
 CTGCAGATGAAGATGGCGCTGGCCATCCTCTTCCGCTTCTACAGCTTCCGGCTGCTGGAG  
 1501 -----+-----+-----+-----+-----+-----+ 1560  
 GACGTCTACTTCTACCGCGACCGGTAGGAGAAGGCGAAGATGTGGAAGGCCGACGACCTC  
 a L Q M K M A L A I L F R F Y S F R L L E -  
 GGGCACCCGGTGCAGTACCGCATGATGACCATCCTCTCCATGGCGCACGGCCTCAAGGTC  
 1561 -----+-----+-----+-----+-----+-----+ 1620  
 CCCGTGGGCCACGTCATGGCGTACTACTGTTAGGAGAGGTACCGCGTGCCGGAGTTCAG  
 a G H P V Q Y R M M T I L S M A H G L K V -  
 CGCGTCTCTAGGGCCGTCTGATGTCATGGCGATTTGGATATGGATATCGTCCCGCTTAAT  
 1621 -----+-----+-----+-----+-----+-----+ 1680  
 GCGCAGAGATCCCGGCAGACTACAGTACCGCTAAACCTATACCTATAGCAGGGCGAATTA  
 a R V S R A V \* C H G D L D M D I V P L N -  
 CCACGACAAATAACGCTCGTGTTACAAATTTGCATGCATGCATGTAAGGGAAAGCGATGG

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1681 -----+-----+-----+-----+-----+ 1740
      GGTGCTGTTTATTGCGAGCACAAATGTTTAAACGTACGTACGTACATTCCCTTTCGCTACC
a      P R Q I T L V L Q I C M H A C K G K R W -
      GTTTCATTGGTGGCTTGGCTTAAGCCTTAAAAACTCCGTCGGGTCTTGCGAACCACCACA
1741 -----+-----+-----+-----+-----+ 1800
      CAAAGTAACCACCGAACCGAATTCGGAATTTTGGAGGCAGCCCAGAACGCTTGGTGGTGT
a      V S L V A W L K P *
      TCACTAGTGTTTTGTACTCTACTCCTCAGTGGGAAGTGTAGTGACAGCATACAAGTTCATC
1801 -----+-----+-----+-----+-----+ 1860
      AGTGATCACAAAACATGAGATGAGGAGTCACCTTCACATCACTGTCGTATGTTCAAGTAG

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                                     XhoI
                                     |
ATATATATTATCCTCTTTCTTAAAAAAAAAAAAAAAAAACTCGAG
1861 -----+-----+-----+-----+----- 1906
      TATATATAATAGGAGAAAGAATTTTTTTTTTTTTTTTTTTGAGCTC

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